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Gencore version 4.5

OM protein - protein search, using sw model

Run on: January 7, 2002, 16:03:53 ; **Search time** 180.87 Seconds
Title: US-08-569-749-8
Perfect score: 267
Sequence: 1 LAKGAEVYIGPGDRVACFAC WEPKDNAMSEHLRHPKCPF 46
Scoring table: BLOSUM62
Gapop 10.0 , gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database :

- 1: SPTRIMBL_17:*
- 2: SP_archea:*
- 3: SP_bacteria:*
- 4: SP_fungi:*
- 5: SP_invertebrate:*
- 6: SP_mammal:*
- 7: SP_minic:*
- 8: SP_organelle:*
- 9: SP_phage:*
- 10: SP_plant:*
- 11: SP_rabbit:*
- 12: SP_ridus:*
- 13: SP_vertebrate:*
- 14: SP_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Length	DB ID	Description
1	267	100.0	1140 4 Q9UNIL	Ogumhi homo sapien
2	232	86.9	589 11 Q9ZC6	09zC6 rattus norv
3	232	86.9	589 11 Q9SEB8	09es8 ratus norv
4	226	84.6	602 11 Q9ES9	09ese9 ratus norv
5	223	83.5	195 13 Q9IA70	09ia70 gallus galli
6	223	83.5	197 13 Q9IA69	09ia69 gallus galli
7	223	83.5	324 13 Q9DDN2	09ddn2 gallus galli
8	223	83.5	610 13 Q9T319	09t319 gallus galli
9	217	81.3	224 11 Q88642	088642 rattus norv
10	175	65.5	496 11 Q9SF0	09sf0 rattus norv
11	175	65.5	501 11 Q9E005	09eq5 rattus norv
12	175	65.5	501 11 Q9E004	09eq4 rattus norv
13	141	52.8	597 11 Q9R015	09r015 mus musculus
14	133.5	50.0	153 5 Q9VEN2	09ven2 drosophila
15	130	48.7	264 12 Q9EN27	09en27 ammacta mao
16	129	48.3	438 5 Q9VU5	09vu5 drosophila
17	126	47.2	377 5 Q9NUJ07	09nu07 spodoptera
18	126	47.2	379 5 Q9UH92	09uh92 trichoplusi
19	124	46.4	281 12 Q9WNL8	09wnl8 choristoneura

הנתקנות - כרך ג' 13

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ALIGNMENTS

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OM protein - protein search, using sw model

Run on: January 7, 2002, 16:03:53 ; Search time 180.87 Seconds
(without alignments)
37.201 Million cell updates/second

Title:	us-08-569-749-8
Perfect score:	267
Sequence:	I LAKAGFYIIGPQDRVACFAC. WEPKDNAMSEHLRHPKCPF 46
Scoring table:	BLOSUM62
	Gapop 10.0 , gapext 0.5
Searched:	473505 seqs, 14627329 residues
Total number of hits satisfying chosen parameters:	473505
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing:	Minimum Match % 100

Result No.	Score	Query Match	Length	DB ID	\$	
					1	2
1	267	100.0	1140	4 Q9UNH1	Q9unh1	homo
2	232	86.9	589	11 Q9QBEC6	Q9gzc6	ratttg
3	232	86.9	589	11 Q9QBEC6	O9ege8	ratttg
4	226	84.6	602	11 Q9SE9	O9ese9	ratttg
5	223	83.5	195	13 Q9IA70	Q9ia70	gallin
6	223	83.5	197	13 Q9IA69	Q9ia69	gallin
7	223	83.5	324	13 Q9DN2	Q9dan2	gallin
8	223	83.5	610	13 Q97319	Q97319	gallin
9	217	81.3	224	11 Q9B642	Q98642	ratttg
10	175	65.5	496	11 Q9ES05	Q9esr0	ratttg
11	175	65.5	501	11 Q9E805	Q9eq05	ratttg
12	175	65.5	501	11 Q9E504	Q9eq04	ratttg
13	141	52.8	597	11 Q9R015	Q9r015	mus
14	133.5	50.0	153	5 Q9VEM2	Q9vem2	drosophila
15	130	48.7	264	12 Q9E97	Q9en27	aminoacids
16	129	48.3	438	5 Q9VOK5	Q9vok5	drosophila
17	126	47.2	377	5 Q9N107	Q9n107	spodoptera
18	126	47.2	379	5 Q9IU92	Q9iu92	trichoplax
19	124	46.4	281	12 Q9INL8	Q9inl8	chorioptera

RT	"Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes."
RL	Submitted (SPP-1999) to the EMBL/GenBank/DBJ databases.
CC	-1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR	EMBL; AF08431; XAG22711; -.
DR	InterPro; IPR01170; BIR.
DR	InterPro; IPR00115; CARD.
DR	InterPro; IPR00181; Znf_ring.
PTM	Pfam; PF00653; BIR; 3.
DR	Pfam; PF00615; CARD; 1.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00238; BIR; 3.
DR	SMART; SM00114; CARD; 1.
DR	SMART; SM00184; RING; 1.
DR	PROSITE; PS01282; BIR_REPEAT_1; 1.
DR	PROSITE; PS00143; BIR_REPEAT_2; 3.
KW	Zinc_Finger; PS50205; CARD; 1.
SQ	SEQUENCE 589 AA; 66777 MW; E6812FEE3EA34142 CRC64;
Query Match	86.9%; Score 232; DB 11; Length 589; Best Local Similarity 84.8%; Pred. No. 5.3e-22; Mismatches 39; Conservatve 2; Indels 0; Gaps 0; RT
Matches	1 LAKAGFYVYGPDDRVACFACGGKLSNWEKDNAMESEHRRHFPCKPF 46
OY	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
Db	176 LAKAGFYVYGPDDRVACFACGGKLSNWEKDNAMESEHRRHFPCKPF 221
RESULT	2
Q9QZC6	PRELIMINARY; PRT; 589 AA.
ID	Q9QZC6; AC 09QZC6; DT 01-MAY-2000 (TREMBLrel. 13, Created) 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	INHIBITOR OF APOPTOSIS PROTEIN 2.
OS	Rattus norvegicus (Rat)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus; NCBI_TaxID=10116; [1]
OX	NCBI_TaxID=10116;
RP	SEQUENCE FROM N.A.
RC	TISSUE="KIDNEY"; RA DONG Z., Denion M., Gu S.M., Saikumar P., Venkatachalam M.A.; EMBL; AF190020; XAF04585; 1; -.
DR	InterPro; IPR001370; BIR.
DR	InterPro; IPR001315; CARD.
DR	InterPro; IPR001441; Znf_ring.
DR	Pfam; PF00653; BIR; 3.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00238; BIR; 3.
DR	SMART; SM00114; CARD; 1.
DR	PROSITE; PS01282; BIR_REPEAT_1; 3.
DR	PROSITE; PS01282; BIR_REPEAT_2; 3.
DR	PROSITE; PS50205; CARD; 1.
KW	Zinc_finger; PS50209; CARD; 1.
SQ	SEQUENCE 589 AA; 66750 MW; B4F7089BD7CD285B CRC64;
Query Match	86.9%; Score 232; DB 11; Length 589; Best Local Similarity 84.8%; Pred. No. 5.3e-22; Mismatches 39; Conservatve 2; Indels 0; Gaps 0; RT
Matches	1 LAKAGFYVYGPDDRVACFACGGKLSNWEKDNAMESEHRRHFPCKPF 46
OY	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
Db	176 LAKAGFYVYGPDDRVACFACGGKLSNWEKDNAMESEHRRHFPCKPF 221
RESULT	4
Q9ESE9	PRELIMINARY; PRT; 602 AA.
ID	Q9ESE9; AC 09ESE9; DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DR	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
OS	Rattus norvegicus (Rat)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus; NCBI_TaxID=10116; [1]
RP	SEQUENCE FROM N.A.
RA	HOLICK M., LeFebvre C.A., Hicks K., Korneluk R.G.; RT "Cloning and Characterization of the Rat Homologs of the Inhibitor of Apoptosis Protein 1, 2, and 3 Genes.";
RT	Submitted (SPP-1999) to the EMBL/GenBank/DBJ databases.
RL	-1 SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
CC	DR EMBL; AF083430; XAG22701; -.
DR	InterPro; IPR01170; BIR.
DR	InterPro; IPR001315; CARD.
DR	InterPro; IPR001441; Znf_ring.
DR	Pfam; PF00653; BIR; 3.
DR	Pfam; PF00619; CARD; 1.
DR	Pfam; PF00097; zf-C3HC4; 1.
DR	SMART; SM00238; BIR; 3.
DR	SMART; SM00114; CARD; 1.
DR	PROSITE; PS01282; BIR_REPEAT_1; 1.
DR	PROSITE; PS01282; BIR_REPEAT_2; 3.
KW	Zinc_finger; PS50209; CARD; 1.
SQ	SEQUENCE 602 AA; 67326 MW; CC91385BEA62DE5A CRC64;
Query Match	84.5%; Score 225; DB 11; Length 602; Best Local Similarity 82.6%; Pred. No. 3.6e-21; Mismatches 38; Conservatve 3; Indels 0; Gaps 0; RT
Matches	1 LAKAGFYVYGPDDRVACFACGGKLSNWEKDNAMESEHRRHFPCKPF 46
OY	01-MAR-2001 (TREMBLrel. 16, Last sequence update)
Db	189 LAKAGFYVYGPDDRVACFACGGKLSNWEKDNAMESEHRRHFPCKPF 234

RESULT	5	PRELIMINARY;	PRT;	195 AA.
ID	Q9IA70			
AC	Q9IA70;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DE	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
INHIBITOR OF APOPTOSIS 1 (FRAGMENT).				
Galiius galius (Chicken).				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.				
OX	NCBI_TAXID=9031;			
RN				
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BREED LECHORN; TISSUE=SPLEEN;			
Zhou H., Lamont S.J.;				
"Genetic variation among chicken lines and mammalian species in specific genes."				
Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.				
EMBL; AF221082; AAC35319.1; -.				
InterPro; IPR001370; BIR.				
PFam; PF00653; BIR; 2.				
SMART; SM0028; BIR; 2.				
DR	PROSITE; PS01243; BIR_REPEAT_2; 2.			
DR	PROSITE; PS01243; BIR_REPEAT_2; 2.			
FT	NON_TER 1			
FT	NON_TER 195 AA; 22347 MW; 9C39BFA755E24E48 CRC64;			
SEQUENCE				
Query Match	83.5%	Score 223;	DB 13;	Length 195;
Best Local Similarity	80.4%	Pred. No. 2.7e-21;		
Matches	37;	Conservative	3;	Mismatches 6;
				Indels 0; Gaps 0;
RESULT	6			
ID	Q9IA69			
AC	Q9IA69;	PRELIMINARY;	PRT;	197 AA.
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DE	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
INHIBITOR OF APOPTOSIS 1 (FRAGMENT).				
Galiius galius (Chicken).				
OX	NCBI_TAXID=9031;			
RN				
RP	SEQUENCE FROM N.A.			
RC	Pedelton C.N., Bargmann W.J., Varadarajan J., Bose H.R. Jr.;			
"The apoptosis inhibitor ch_IAP1 is a direct transcriptional target of v-Rel and c-Rel."				
Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.				
EMBL; AF311289; AAC31236.1; -.				
InterPro; IPR001370; BIR.				
PFam; PF00653; BIR; 3.				
SMART; SM0028; BIR; 3.				
DR	PROSITE; PS01242; BIR_REPEAT_1; 1.			
DR	PROSITE; PS01243; BIR_REPEAT_2; 3.			
FT	NON_TER 324 AA; 324 MW; 5B2B89DDEA3733F3 CRC64;			
SEQUENCE	324 AA;	36567 MW;	5B2B89DDEA3733F3 CRC64;	
Query Match	83.5%	Score 223;	DB 13;	Length 324;
Best Local Similarity	80.4%	Pred. No. 4.6e-21;		
Matches	37;	Conservative	3;	Mismatches 6;
				Indels 0; Gaps 0;
RESULT	8			
ID	Q57319			
AC	Q57319;	PRELIMINARY;	PRT;	610 AA.
DT	01-JUN-1998 (TREMBLrel. 06, Created)			
DE	01-JUN-1998 (TREMBLrel. 06, Last sequence update)			
INHIBITOR OF APOPTOSIS PROTEIN 1 (IAP) (INHIBITOR OF T CELL APOPTOSIS PROTEIN).				
GN	IAP1.			
OS	Galiius galius (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-BREED FRYOMI; TISSUE=SPLEEN;			
RA	Zhou H., Lamont S.J.;			
RT	"Genetic variation among chicken lines and mammalian species in specific genes."			
RT	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AF221083; AAC35320.1; -.			
DR	InterPro; IPR001370; BIR.			
PFam; PF00653; BIR; 2.				
SMART; SM0028; BIR; 2.				
PROSITE; PS01242; BIR_REPEAT_1; 2.				
PROSITE; PS01243; BIR_REPEAT_2; 2.				
FT	NON_TER 1 AA; 1 MW; 17328-73411997.			
FT	NOL_TER 197 AA; 197 MW; D7923DABC623B1A CRC64;			
SEQUENCE				
CC	- FUNCTION: SUPPRESSOR OF APOPTOSIS IN ONCOPROTEIN V-REL-TRANSFORMED CELLS.			

CC	-1 - TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN THE SPLEEN, THYMUS, BURSA, INTESTINE, AND LUNG, AND AT VERY LOW LEVELS IN TESTIS, BRAIN, AND SKELETAL MUSCLE.
CC	-1 - INDUCTION: INDUCED DURING THE V-REL-MEDIATED TRANSFORMATION
CC	-1 - DOMAIN: THE RING FINGER IS IMPORTANT FOR ITS ANTIAPOPTOTIC EFFECT.
CC	-1 - SIMILARITY: MEMBER OF THE IAP FAMILY.
CC	-1 - SIMILARITY: CONTAINS 3 BIR DOMAINS (BACULOVIRAL INHIBITION OF APOPTOSIS PROTEIN REPEAT).
CC	-1 - SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.
DR	EMBL: AF008592; AAC88044; 1; -
DR	HSSP: 01390; 1QBH.
DR	InterPro: IPRO01370; BIR.
DR	InterPro: IPRO01315; CARD.
DR	InterPro: IPRO01841; Zinc_finger.
DR	Pfam: PF0053; BIR; 3.
DR	Pfam: PF00319; CARD; 1.
DR	Pfam: PF00097; zf-C3HC4; 1.
DR	SMART: SM00114; CARD; 1.
DR	SMART: SM00184; RING; 1.
DR	PROSITE: PS01282; BIR_REPEAT_1; 3.
DR	PROSITE: PS50209; CARD; 1.
KW	Apoptosis; Zinc-finger; Repeat.
FT	REFSET 30 97 BIR_REPEAT 1.
FT	REFSET 175 242 BIR_REPEAT 2.
FT	REFSET 262 329 BIR_REPEAT 3.
FT	ZN FING 563 597 C3HC4-TYPE.
SQ	SEQUENCE 610 AA: 68924 MW: ADFV7619650BA44A6 CRC64;
RESULT 9	Query Match 83.5%; Score 223; DB 13; Length 610; Best Local Similarity 80.4%; Pred. No. 9e-21; Matches 37; Conservative 3; Mismatches 6; Indels 0; Gaps 0; OQ 1 LAKAGPYIIGFDRVACAGGGKLSWEPKDNAMSEHLRHFPCPF 46 Db 196 LAKAGLYIIGDADKVACFGCGQLSNWEPKDNAMSEHRRHFPCPF 241
088642	PRELIMINARY; PRT; 224 AA.
ID	088642; 088642; 088642;
AC	088642; 088642; 088642;
DT	01-NOV-1998 (TREMBLrel. 08, Created) 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-NOV-2001 (TREMBLrel. 17, Last annotation update)
DE	INHIBITOR OF APOPTOSIS PROTEIN (FRAGMENT).
GN	RAT1.
OS	Rattus norvegicus (Rat); Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RC	STRAIN=10116; STRAIN=WISTAR; TISSUE=OVARY; CORPUS LUTEUM;
RA	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherilia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RT	Cloning and characterization of an inhibitor of apoptosis protein (IAP) in the rat corpus luteum.;
RL	Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
DR	EMBL: AF08153; AAC32497; 1; -
DR	HSSP: Q1390; 1QBH.
DR	InterPro: IPRO01370; BIR.
DR	Pfam: PF0053; BIR; 2.
DR	SMART: SM00238; BIR; 2.
DR	PROSITE: PS50143; BIR_REPEAT_2; 3.
FT	NON_TER 1 1
FT	SEQUENCE 224 AA; 25209 MW: 213A52534D5BB56A CRC64;
RESULT 10	Query Match 81.3%; Score 217; DB 11; Length 224; Best Local Similarity 78.3%; Pred. No. 1.9e-20; Matches 36; Conservative 2; Mismatches 8; Indels 0; Gaps 0; OQ 1 LAKAGPYIIGFDRVACAGGGKLSWEPKDNAMSEHLRHFPCPF 46 Db 105 LGKAAPYIIGDADKVACFGCGQLSNWEPKDNAMSEHRRHFPCPF 150
098050	PRELIMINARY; PRT; 496 AA.
ID	098050; 098050;
AC	098050; 098050;
DT	01-MAR-2001 (TREMBLrel. 16, Created) 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE	INHIBITOR OF APOPTOSIS PROTEIN 3.
OS	Rattus norvegicus (Rat); Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherilia; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RA	NCBI_TaxID:10116;
RC	SEQUENCE FROM N.A.
RA	STRAIN=WISTAR; TISSUE=OVARY;
RA	Lareu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmarajan A.M.;
RT	"Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum.";
RT	Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
CC	-1 - SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.
DR	EMBL: AF30433; AAC4192; 1; -
DR	InterPro: IPRO01370; BIR.
DR	InterPro: IPRO01841; Zinc_finger.

DR	Pfam: PF00653; BIR: 3.	OX	NCBI_TaxID=10090;
DR	Pfam: PF00653; zf-CCHC4; 1.	RN	{1}
DR	SMART: SM00238; BIR: 3.	RP	SEQUENCE FROM N. A.
DR	SMART: SM00184; RING: 1.	RX	MEDLINE=9431676; PubMed=10501978;
DR	PROSITE: PS01282; BIR_REPEAT_2; 3.	RA	Huang S., Schatz J.M., Crowley J.D., Endrizzi M.G., Dietrich W.F.;
KW	ZINC-FINGER.	RT	"the mouse Nail gene cluster on Chromosome 13 encodes several distinct functional transcripts."
SQ	SEQUENCE 501 AA: 56548 MW: 9973FBF28E81C5AO CRC64;	RA	Macm. Genome 10:1032-1035(1999).
DR	184 LASAGLYVYTGIDQVOCFCGGGLKNNPCDRAWSEHRRHFPNCFF 229	DR	EMBL: AF15493; AAD56765.1; -.
RESULT	12	DR	HSRP; Q13490; IQBP1.
ID	QB004 PRELIMINARY; PRT; 501 AA.	DR	MGB; Q011298220; Bircle.
ID	Q9E0D4 PRELIMINARY; PRT; 501 AA.	DR	InterPro: IPR01370; BIR.
AC	Q9E0D4	DR	Pfam: PF00653; BIR: 3.
DT	01-MAR-2001 (TREMBREL, 16, Created)	DR	SMART: SM00238; BIR: 3.
DT	01-MAR-2001 (TREMBREL, 16, last sequence update)	DR	PROSITE: PS01282; BIR_REPEAT_2; UNKNOWN_2.
DT	01-JUN-2001 (TREMBREL, 17, Last annotation update)	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DE	INHIBITOR OF APOPTOSIS PROTEIN 3.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
OS	Rattus norvegicus (rat).	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
OC	Eukaryota; Metazoa; chordata; Craniata; vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
OX	NCBI_TaxID=10116;	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RN	[1]	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RP	SEQUENCE FROM N. A.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RC	STRAIN=WISTAR; TISSUE=OVARY;	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RA	Larieu R.R., Bradley C.K., Lacher M., Friis R.R., Dharmaratna A.M.; "Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum"; Submitted (SPP-2000) to the EMBL/GenBank/DBJ databases.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RT	-I - SIMILARITY: CONTAINS A RING-TYPE ZINC FINGER.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RL	EMBL: AP04334; AAC41193; 1; -.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
CC	INTERPRO: IPR01370; BIR.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	INTERPRO: IPR001370; BIR.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	INTERPRO: IPR001370; BIR.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	INTERPRO: IPR001370; BIR.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	INTERPRO: IPR001370; BIR.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	PFAM: PF00653; BIR; 3.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	PFAM: PF00653; BIR; 3.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	SMART: SM00238; BIR; 3.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	PROSITE: PS01282; BIR_REPEAT_1; 1.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DR	PROSITE: PS01282; BIR_REPEAT_2; 3.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
KW	ZINC-FINGER.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
SQ	SEQUENCE 501 AA: 56578 MW: 4863369FF2EDC8CD CRC64;	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RP	SEQUENCE FROM N. A.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RC	STRAIN=BERKELEY;	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RA	MEDLINE=20196006; PubMed=10731132;	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RA	Adams M.D., Ceinier S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherzer S.E., Li P.W., Heskies R.A., Galle R.F., George R.A., Lewis S.E., Richards M.D., Henderson S.N., Sutton G.J., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.J., Winkler J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blaize R.G., Champe M., Pfleiderer B.D., Wan K.-H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.I.G., Abril J.F., Agayam A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballou R.M., Beszu A., Baxendale J., Bayaktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Bernick B.P., Bhandari D., Bolshakov S., Borikova D., Botchan M.R., Bouck J., Brokstein P., Brodtier P., Brottier P., Burrows K.C., Busam D.A., Buttler J.H., Cadile E., Centner A., Chandra T., Cherry J.M., Cowley S., Dahlie C., Davenport U.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Dobson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R., Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W., Foster C., Gabril A.E., Garg N.S., Gelbart W.M., Glaser K., Gladzik A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwam C., Jalali M., Kalush F., Karpen G.R., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz C., Kulp D., Lai Z., Lasko P., Leij Y., Levitt A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Mathei T.C., McIntosh M.P., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mohrly C., Morris J., Moskoff A., Mount S.M., Moy M., Murphy B., Murphy L., Muzyk D.M., Nelson D.L., Nelson D.R., Nixon K., Nixon D.R., Pacileo J.M., Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
RESULT	13	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
ID	Q9R015 PRELIMINARY; PRT; 597 AA.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
AC	Q9R015	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DT	01-MAY-2000 (TREMBREL, 13, Created)	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DT	01-MAY-2000 (TREMBREL, 13, Last sequence update)	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DT	01-JUN-2001 (TREMBREL, 17, Last annotation update)	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
DE	NEURONAL APOPTOSIS INHIBITORY PROTEIN.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
GN	BIRCLE OR HAIR.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
OS	Mus musculus (Mouse).	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.
OC	Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorphi; Muridae; Murinae; Mus.	DR	PROSITE: PS01282; BIR_REPEAT_2; 3.

Rainey K., Remington I., Saunders R. D. C., Scheeler F., Shen H., Shue B. C., Skinner J., Skupski M. P., Smith T., Spier B., Spradling A. C., Stickleton M., Strong R., Sun E., Swanson R., Tector E., Turner E., Wang R. H., Wang X.,

Search completed: January 7, 2002, 16:03:53

RA Williams S.-M., Woodage T., Wu D., Yang S., Yao Q.-A.,
 YE J., Yeh R.-F., Zeng J., Zhan M., Zhang G., Zhao O., Zheng L.,
 Zheng X.-H., Zhong N.-N., Zhong W., Zhou K., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*";
 SCIENCE 207:2185-2193 (2000).
 EMBL: AE003716; DR;
 DR HSPB: 013490; 10BR;
 DR Flybase: FBgn0038489; CG12265.
 DR InterPro: IPR001370; BIR.
 DR Pfam: PF00653; BIR; I.
 DR PROSITE: PS00238; BIR; I.
 DR SMART: PS50143; BIR; REPEAT_2; I.
 SQ SEQUENCE: 153 AA; 17455 MW; ED2250EB3B669EC3359 CRC64;

Query Match Similarity 50.0%; Score 133.5; DB 5; Length 153;
 Best Local Match 44.9%; Pred. No. 8; ge=10;
 Matches 22; Conservative 8; Mismatches 16; Indexes 3; Gaps 1

REB037
ID Q9EN27
AC Q9EN27;
PRELIMINARY; PRT; 264 AA.

DT 01-MAR-2001 (Tremblei, 16; last sequence update)
DT 01-JUN-2001 (Tremblei, 17; last annotation update)
DE AMY021.
GN

VIRUSES: USUALLY VIRUSES, NO RNA STAGE; ENTOPOXVIRIDAE; ENTOPOXVIRINAE;
OC: ENTOPOXVIRUS B;
OC: ENTOMOPOTVIRUS;
OX: NCBI-TAXID=28321;
RN: [1]

R.A.
RA
Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
Moyer R.W.,
"Complete Genomic Sequence of the *Amsacta moorei* Entomopoxvirus:

NU
VIOLOGY 27:1140-1159 (2000).
RN
[2]
RP
SEQUENCE FROM N.A.
RA
Bawden A.L., Glaesberg K.J., Diggans J., Shaw R., Farmerie W.,

STANDARDIZED DATA MODEL FOR THE SEMI-STRUCTURED
EMBODIED APPLICABILITY OF THE SEMI-STRUCTURED
INTERPRO: IPR001300; BIR.
INTERPRO: IPR001841; BIR.
DR

DR SPONI; PROTOC; RING; 1.
PRONI; PROTOC; RING; 2.
BIR_REPEAT_2; 2.
SEQUENCE: PS50143; BIR_REPEAT_2;
SO 264 AA; 30547 MW; 2EB72DA4B58D920A CRC64;

Query Match 48.7%; Score 130; DB 12; Length 264;
Best Local Similarity 47.8%; Pred. No. 4; 5e-09;
Matches 22; Conservative 7; Mismatches 17; Indels 6

Tue Jan 8 08:23:54 2002

us-08-569-749-8.rspt

